

FIGURE 1

1 AGCTCCAGCCTAGGCGTTCTACCTGGAAAGATGCAGGGGCCAGTACCTAGGACTGAGGA 60
61 AGATGGCTGACATCCAGAACAATTCGCTGGACAGCCAGGAGCGTAGGGCTGTGGCAG 120
121 TGCCCTGATCTTTGCCCTCAATCTTCCTGTGGCAATGGTGGCAATGGGCTGGTGTGG 180
181 CTGTGCTACTGCAGCCTGGCCCAAGTGCCCTGGCAGGAGCCAAAGCAGTACCCACAGATCTCT 240
241 TCATCCTCAACTTGGCCGTGGCCGACCTTTGGCTTCATCTGTGCTGCAAGACGGTACATC 300
301 CAGCCATCTACACACTGGATGCCCTGGCTCTTTGGGCTTTTCGCTGTGCAAGACGGTACATC 360
361 TGCTCATCTACCTACCATGTATGCCAGCAGCTTCACCCCTGGCGGCCGTCTCCCTGGACA 420
421 GGTACCTGGCTGTGGCACCCACTGCGCTCCAGAGCCCTGCGCACCCCGCGCAACGCGC 480
481 GCGCCGCGTGGGCTCGTGTGGCTGCTGGCGGCTCTCTTTTCGCGGCCCTACCTAAGCT 540
541 ATTACGGCACGGTGCCTACGGCGGCTCGAGCTCTGCTGCGGCCGTGGGAGGACGCGC 600
601 GGCGCGCGCTGGACGTGGCCACCTTCGCCCGGGCTACCTGCTGCCGGTCCCGGGCG 660
661 TGAGCCTGGCTACGGACGACCGCTATGTTTCCATATGGCCCGCGGAGCGCCATGCTGGCAG 720
721 CGCGGGCAGCAGAGCGCGCAGACGGCGACCGCGCGGCGGAGCGCCATGCTTCTGGT 780
781 TGGCGCGCTTACGCGCTTTGCTGGGCGCCGACACGCGCTCATCTCTGCTTCTGCTCG 840
841 ACGGCCGCTTCAGCCCGGCCACCTACGCTGTGCGCTGCGCTCGCGCCACTTCCGCG 900
901 CCTACGCCAATCCTGCTTAACCCGCTCGTCTACTGCTGCGCTCGCGCCACACCGCGCTC 960
961 CGCGCTTCGCGCGCTGTGGCCCTGCGCGCTCGCGCCACCGCCACACCGCGCGCTC 1020
1021 ATCGAGCCCTCCGTGCTGTCAGCCCGCGCTCTCGGGCCCGCGCGCTATCCCGCGGACG 1080
1081 CCAGGCCCTCGTGGAGTATGAGCCAGAGGGGATGCTCTGCGTGTGGTGGAGAGA 1140
1141 CTAGACTAACCCCTGTCCCGGAGGACCTCAATAACCCCTGCCCGCTTGGACTCTGACGTC 1200
1201 TGTCAAGATGCCACCAAGGAACATCTAGGGAACGGCAGTCTCGCCAGGCTCCACCAAAA 1260
1261 GCAGAGCAAAAGTTGCAGGG 1280

FIGURE 2

20	V	A	F	A	L	R	R	Y	R	V	A	V	Y	A	A	H	A	T
40	A	L	L	Q	H	D	A	S	A	V	G	A	W	L	R	A	D	E
60	V	V	D	F	V	L	N	L	D	A	A	L	F	C	F	R	G	G
80	A	L	T	P	T	S	R	Y	E	V	P	M	C	H	H	H	P	G
100	G	G	T	V	K	V	P	P	W	P	G	A	L	S	R	H	Y	G
120	V	N	S	C	C	A	T	A	A	L	V	R	I	A	S	H	G	R
140	S	G	S	C	V	A	R	S	P	L	A	G	L	L	A	R	A	L
160	G	V	P	L	F	L	L	F	V	Y	A	A	A	R	L	H	P	A
180	P	M	E	I	A	T	A	L	C	G	W	R	H	C	S	R	G	D
200	S	G	Q	F	G	F	R	A	L	A	L	G	H	A	Y	R	S	G
220	D	L	W	C	F	S	S	A	E	A	F	T	P	Y	V	R	S	R
240	L	L	A	L	L	S	R	L	L	F	C	A	G	T	L	G	A	P
260	S	F	S	D	W	A	L	L	A	T	L	R	W	A	P	C	P	E
280	I	I	P	A	A	Y	P	W	G	A	T	R	C	P	N	P	Q	M
300	N	L	G	V	D	M	H	V	Y	V	R	R	L	S	L	W	V	S
320	Q	A	P	A	L	T	R	L	R	D	G	A	A	F	C	L	R	W
340	I	F	Q	L	T	L	V	G	V	L	Y	E	Y	A	S	R	R	G
360	D	I	L	N	Y	Y	A	V	T	A	A	A	L	F	N	R	L	R
370	A	V	L	L	I	I	L	A	G	R	L	A	A	R	A	F	A	P
	M	P	V	I	A	L	Y	A	Y	R	S	A	A	G	Y	R	R	R

FIGURE 3

1	CACTCAGCGATGACTTTGGCTCTGCTCTCCCCCTCCCTCCATCTCCACGAGCTTCCAGCCC	60
61	AGAACACCTGGCCAGACCCAGGTCGGGGAGTTAGATCCCGGGGTCAAGCAACCAGAACT	120
21	GGGGCTCTTGCCCTGAGGATTCACGCTTCTCTTCCAGGTGCCCTCTGATGGGAGATG	180
81	GCTGATGCCCAGAACATTTCACTGGACAGCCAGGAGTGTGGGGGCCGTGGCAGTGGCTT	240
141	GTGGTCTTTGCCCTAATCTTCTTCCCTGGGACAGTGGGCAATGGGCTGGTGCITGGCAGTIG	300
161	CTCCTGCAGCCCTGGCCCGAGTGCCCTGGCAGGAGCCTGGCAGCACCAAGGACCTGTTCATC	360
181	CTCAACCTGGCGGTGGCTGACCTCTGCTTCACTCCTGTGCTGCGTGGTGGCTTCCAGGCCACC	420
201	ATCTACACGCTGGATGCCCTGGCTCTTTGGGGCCCTCGTCTGCAAGGCCCTGCACCTGCTC	480
221	ATCTACCTACCATGTACGCCAGCAGCTTTACGCTGGCTGCTGTCTCCCTGGACAGGTAC	540
241	CTGGCCGTGGGCAACCGCTGGCTCGCGGCCCTGCGACGCCCGCTAACGCCCGCGCC	600
261	GCAAGTGGGCTGGTGGCTGCTGGCGGCGCTCTTCTCGGCGCCCTACCTCAGCTACTAC	660
281	GGACCCGTGGCTACGGCGGCTGGAGCTCTGCTGCCCGCTGCGAGGAGCGCGCGCGC	720
301	CGGCCCTGACGTGGCCACCTTCGCTGCCGCTACCTGCTGCCCTGGGCTGGTGGTGAGC	780
321	CGGCCCTGACGTGGCCACCTTCGCTGCCGCTACCTGCTGCCCTGGGCTGGGCTGGGCG	840
341	CTGGCCCTACGGCGGACGCTGGCTTCCCTGGGCGCGCTGGTCCCGCGCGGCTGGCC	900
361	GCGGCCGAGGCGCGGAGGGCGACGGGCGCGCGGCGGCTCATCTGTGCTTCTGTGTACGGC	960
381	GCGCTCTACGCGCTCTGTGGGTCCGACCAACGCGCTCATCTGTGCTTCTGTGTACGGC	1020
401	CGCTTCGCCCTTACGCCCGGCCACCTACGCTGCCGCTGGCCCTCACACTGCCCTGGCCCTAC	1080
421	GCCAACTCCTGCTCAACCCGCTCGTCTACGCGCTCGCTCGGCCACTTCCGCGCGCGC	1140
441	TTCCCGCGGCTGTGGCCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	1200
461	CGCGTCCGCGCGGCTCTCGGGCCCAACCCGCTGCCCGGAGACGCCCGCGCGCGCGCGGA	1260
481	AGGCTGCTGGCTGGTGGCGGCGAGGCCCGGAGCCAGGAGGAGGCCGTCACCGCGCGA	1320
501	GAGGCTGCCCGAGGACCGGAATAAACCTTCCCGCTGGACTCCGCTGTGTCCGCTCTGTC	1380
521	TCACTCCCGTCTCCGAAGGCGGACGCCACCGGGCCAGGATGGGGCAATGCCACGAGC	1417
541	TCTCTAGGGCGCTTGAGTGGAGCGACTTGTCCCCCGC	

FIGURE 4

P	T	M	V	I	T	L	A	R	S	A	G	Y	R	R	G
Q	R	E	V	A	F	A	L	R	Y	R	V	A	V	A	L
F	T	G	A	L	L	Q	H	D	A	S	A	V	G	A	W
S	A	D	V	V	D	F	V	N	L	D	A	A	L	F	C
T	Q	S	A	L	T	P	A	S	R	Y	E	V	P	M	C
P	G	P	G	G	T	V	K	V	P	P	W	P	G	A	L
S	R	C	V	N	S	C	C	A	T	A	A	L	V	R	I
P	S	R	S	G	G	C	V	A	R	S	P	L	A	G	L
P	R	P	G	V	P	L	L	L	L	F	V	Y	A	A	R
P	V	L	P	T	E	I	A	T	A	L	C	G	W	R	H
S	G	S	S	G	Q	F	G	F	R	A	L	A	L	G	H
L	G	A	D	L	W	C	F	S	S	A	E	A	F	T	P
L	V	P	L	L	A	L	L	S	R	L	L	F	R	A	G
A	Q	I	S	F	S	D	W	A	L	L	A	T	L	R	W
L	T	R	I	I	P	A	A	Y	P	W	G	A	T	R	C
T	Q	L	N	L	G	V	D	M	H	V	Y	V	R	R	L
M	G	C	Q	A	P	A	L	T	R	L	R	D	G	A	A
A	P	S	A	F	Q	L	T	L	V	G	V	L	Y	E	Y
S	T	G	D	V	L	N	Y	Y	A	V	T	A	A	A	L
H	R	G	A	V	L	L	I	I	L	A	G	R	L	A	A

FIGURE 5A

hGALR3	M A D A Q N I S L D S P G	13
rGALR3	13
rGALR1	M E L A P V N L S E G N G S D P E P P A E P R P L		25
<hr/>			
hGALR3	S V G A V A V P V V F A L I F L L G T V G N	35
rGALR3	35
rGALR1	F G I G V E N F I T L V V F F A M G V L G N		50
<hr/>			
hGALR3	G L V L A V L L Q P G P S A W Q E P G S T T D L F		60
rGALR3	G L V L A V L L Q P G P S A W Q E P S S T T D L F		60
rGALR1	S L V I T V L A R S K P G . . . K P R S T T N L F		72
<hr/>			
hGALR3	I L N L A V A D L C F I L C C V P F Q A T I Y T L		85
rGALR3	I L N L A V A D L C F I L C C V P F Q A T I Y T L		85
rGALR1	I L N L S I A D L A Y L L F C I P F Q A T V Y A L		97

FIGURE 5B

	III																										
hGALR3	D	A	W	L	F	G	A	L	V	C	K	A	V	H	L	L	L	I	Y	L	T	M	Y	A	S	S	110
rGALR3	D	A	W	L	F	G	A	F	V	C	K	T	V	H	L	L	L	I	Y	L	T	M	Y	A	S	S	110
rGALR1	P	T	W	V	L	G	A	F	I	C	K	F	I	H	Y	F	F	T	V	S	M	L	V	S	I		122
hGALR3	F	T	L	A	A	V	S	V	D	R	Y	L	A	V	R	H	P	L	R	S	R	A	L	R	T		135
rGALR3	F	T	L	A	A	V	S	L	D	R	Y	L	A	V	R	H	P	L	R	S	R	A	L	R	T		135
rGALR1	F	T	L	A	A	M	S	V	D	R	Y	V	A	I	V	H	S	R	S	S	S	L	R	V			147
hGALR3	P	R	N	A	R	A	A	V	G	L	V	W	L	L	A	A	L	F	S	A	P	Y	L	S	Y		160
rGALR3	P	R	N	A	R	A	A	V	G	L	V	W	L	L	A	A	L	F	S	A	P	Y	L	S	Y		160
rGALR1	S	R	N	A	L	L	G	V	G	F	I	W	A	L	S	I	A	M	A	S	P	.	V	A	Y		171
hGALR3	Y	G	T	V	.	.	R	Y	G	A	L	E	L	C	V	P	A	W	.	E	D	A	R	R	R		182
rGALR3	Y	G	T	V	.	.	R	Y	G	A	L	E	L	C	V	P	A	W	.	E	D	A	R	R	R		182
rGALR1	Y	Q	R	L	F	H	R	D	S	N	Q	T	F	C	W	E	H	W	P	N	Q	L	H	K	K		196

FIGURE 5C

hGALR3	A	L	D	V	A	T	F	A	A	G	Y	L	L	P	V	A	V	V	S	L	A	Y	G	R	T	207	
rGALR3	A	L	D	V	A	T	F	A	A	G	Y	L	L	P	V	A	V	V	S	L	A	Y	G	R	T	207	
rGALR1	A	Y	V	V	C	T	F	V	F	G	Y	L	L	P	L	L	L	I	C	F	C	Y	A	K	V	221	
hGALR3	L	R	F	L	W	A	A	V	G	P	A	G	A	A	A	A	E	A	R	R	R	A	T	G	R	232	
rGALR3	L	C	F	L	W	A	A	V	G	P	A	G	A	A	A	A	E	A	R	R	R	A	T	G	R	232	
rGALR1	L	N	H	L	H	K	K	L	K	N	M	S	K	K	S	E	A	S	K	K	K	242	
hGALR3	A	G	R	A	M	L	A	V	A	A	L	Y	A	L	C	W	G	P	H	H	A	L	I	L	C	257	
rGALR3	A	G	R	A	M	L	A	V	A	A	L	Y	A	L	C	W	G	P	H	H	A	L	I	L	C	257	
rGALR1	T	A	Q	T	V	L	V	V	V	V	V	F	G	I	S	W	L	P	H	H	V	I	H	L	W	267	
hGALR3	F	W	Y	G	R	F	F	A	F	S	P	A	T	Y	A	C	R	L	A	S	H	C	L	A	Y	A	282
rGALR3	F	W	Y	G	R	F	F	A	F	S	P	A	T	Y	A	C	R	L	A	S	H	C	L	A	Y	A	282
rGALR1	A	E	F	G	A	F	F	L	T	P	A	S	F	F	F	R	I	T	A	H	C	L	A	Y	S	292	

FIGURE 5D

hGALR3	N	S	C	L	N	P	L	V	Y	A	L	A	S	R	H	F	R	A	R	F	R	R	L	W	P	307
rGALR3	N	S	C	L	N	P	L	V	Y	S	L	A	S	R	H	F	R	A	R	F	R	R	L	W	P	307
rGALR1	N	S	S	V	N	P	I	I	Y	A	F	L	S	E	N	F	R	K	A	Y	K	Q	V	F	K	317
hGALR3	C	G	R	R	R	.	.	.	R	H	R	A	R	R	A	L	R	R	V	R	P	A	S	S	G	329
rGALR3	C	G	R	R	R	H	R	H	H	R	A	H	R	A	L	R	R	V	Q	P	A	S	S	G	332	
rGALR1	C	R	V	C	N	E	S	P	H	G	D	A	K	E	K	N	R	I	D	T	P	P	S	T	N	342
hGALR3	P	P	G	C	P	G	D	A	R	P	S	G	R	L	L	A	G	G	Q	G	P	E	P	R	354	
rGALR3	P	A	G	Y	P	G	D	A	R	P	R	G	W	S	M	E	P	R	350	
rGALR1	C	T	H	V	346	
hGALR3	E	G	P	V	H	G	G	E	A	A	R	G	P	E				368		
rGALR3	G	D	A	L	R	G	G	E	T	R	L	T	L	S	P	R	G	P	Q					370		

FIG. 6A

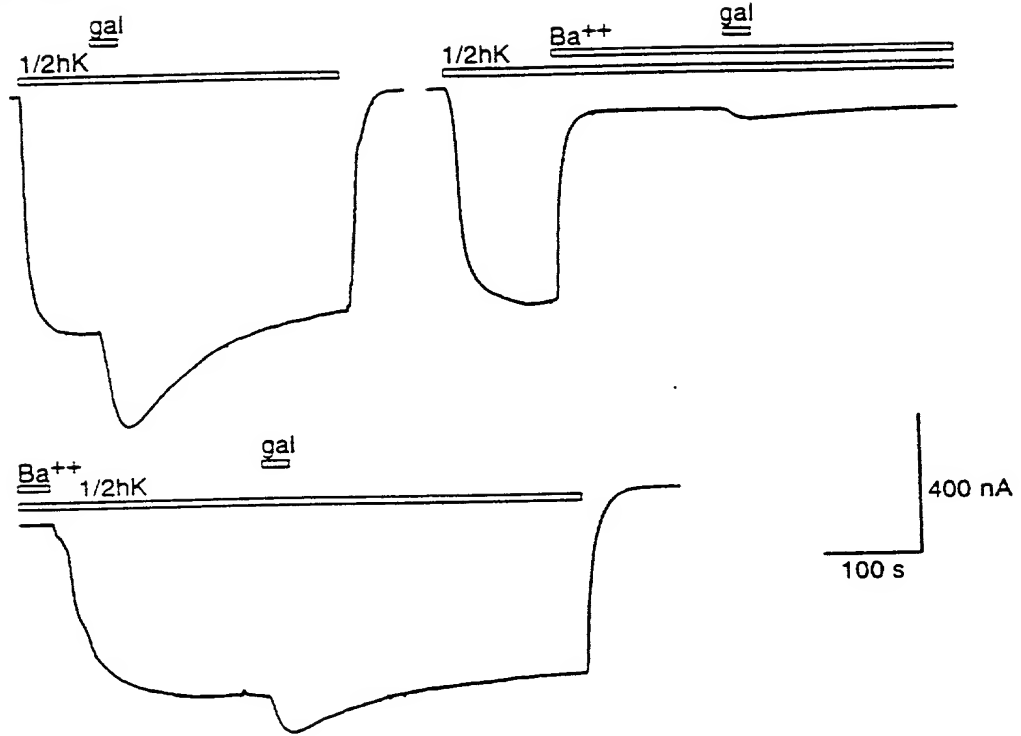


FIG. 6B

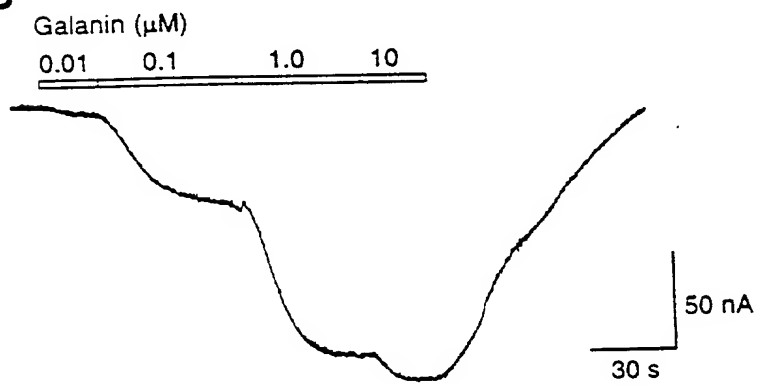


FIG. 7

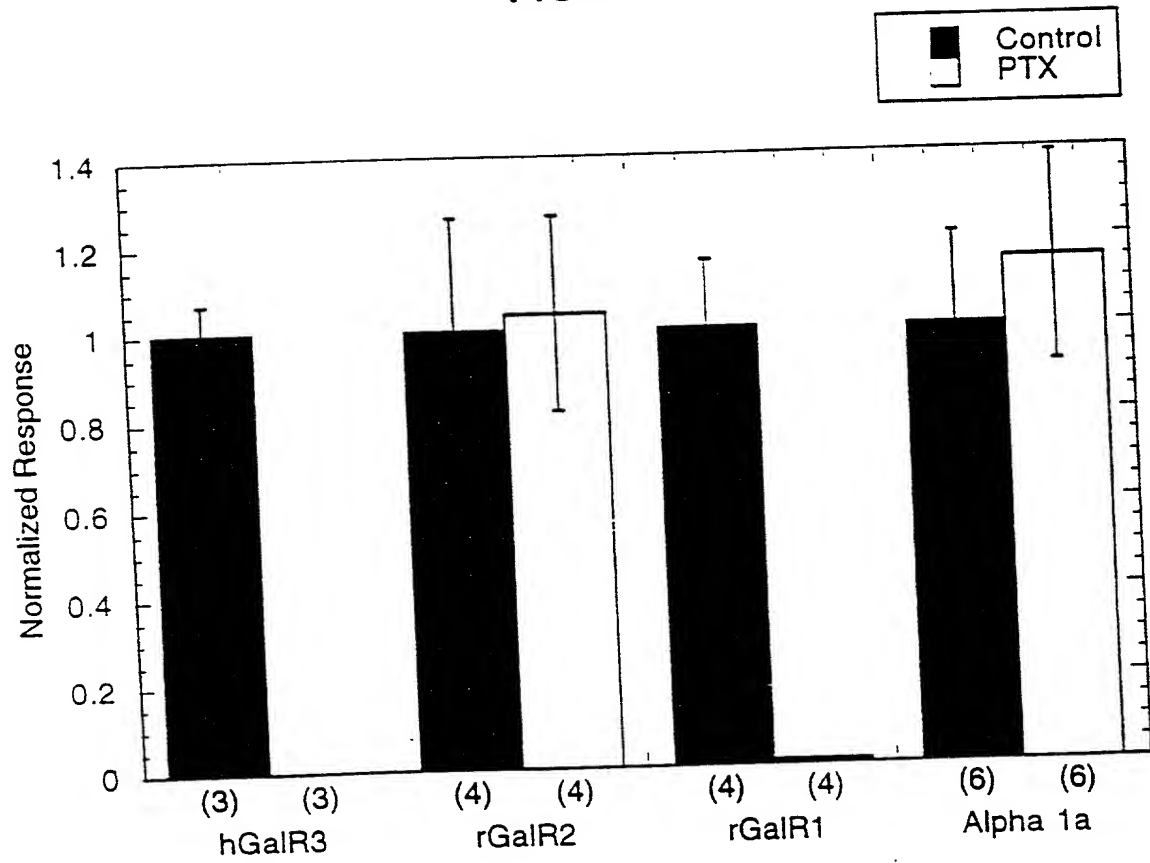


FIG. 8A

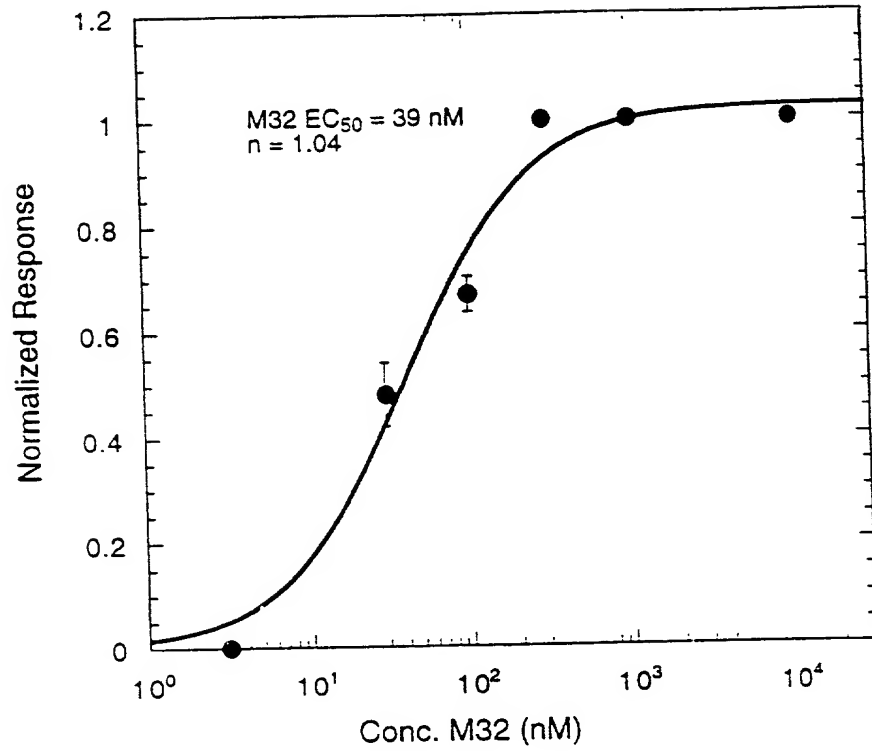


FIG. 8B

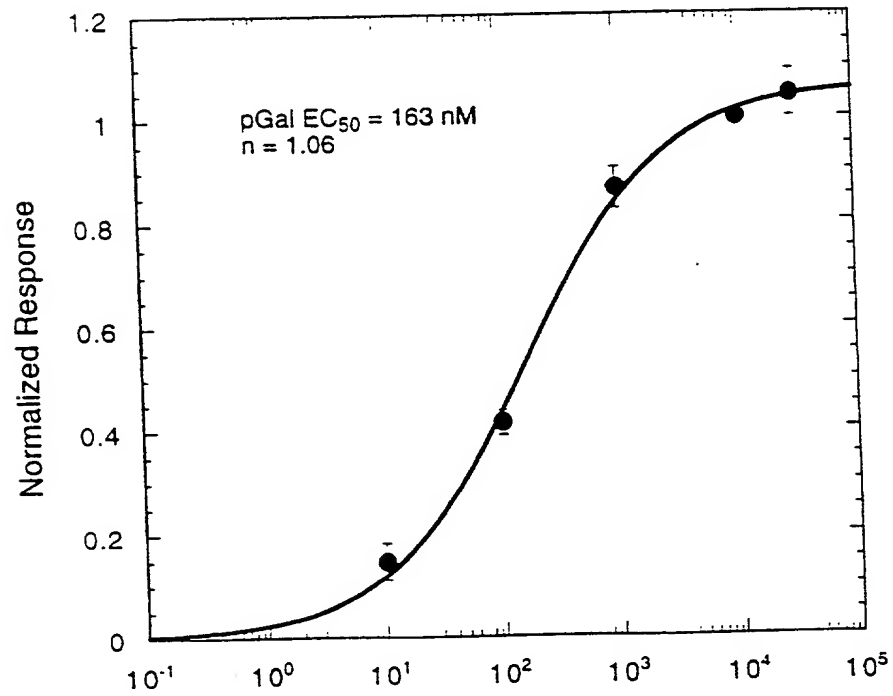


FIG. 8C

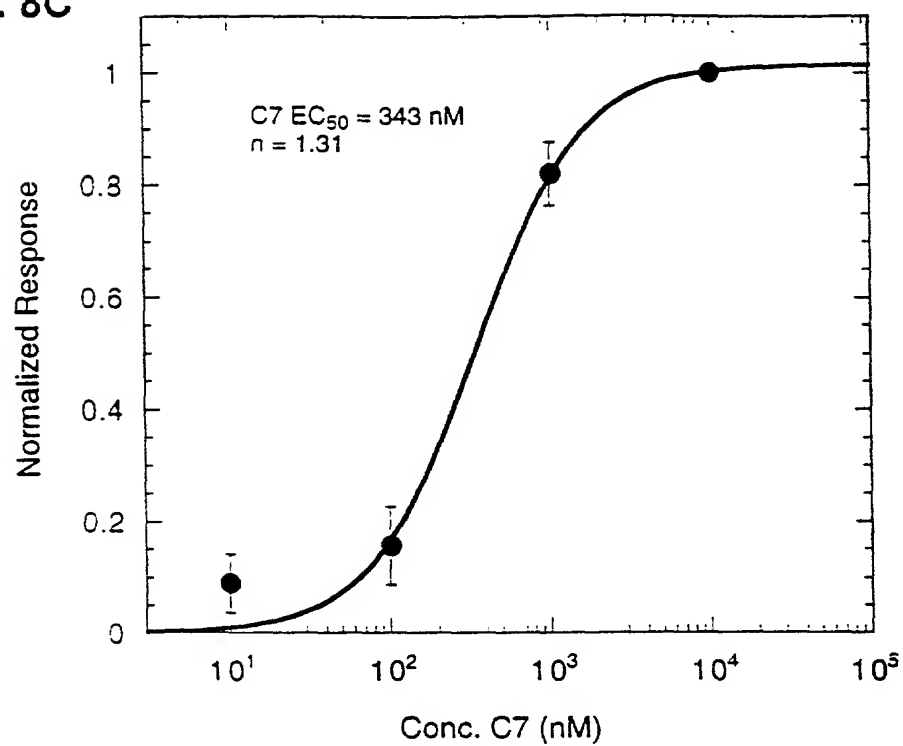


FIG. 8D

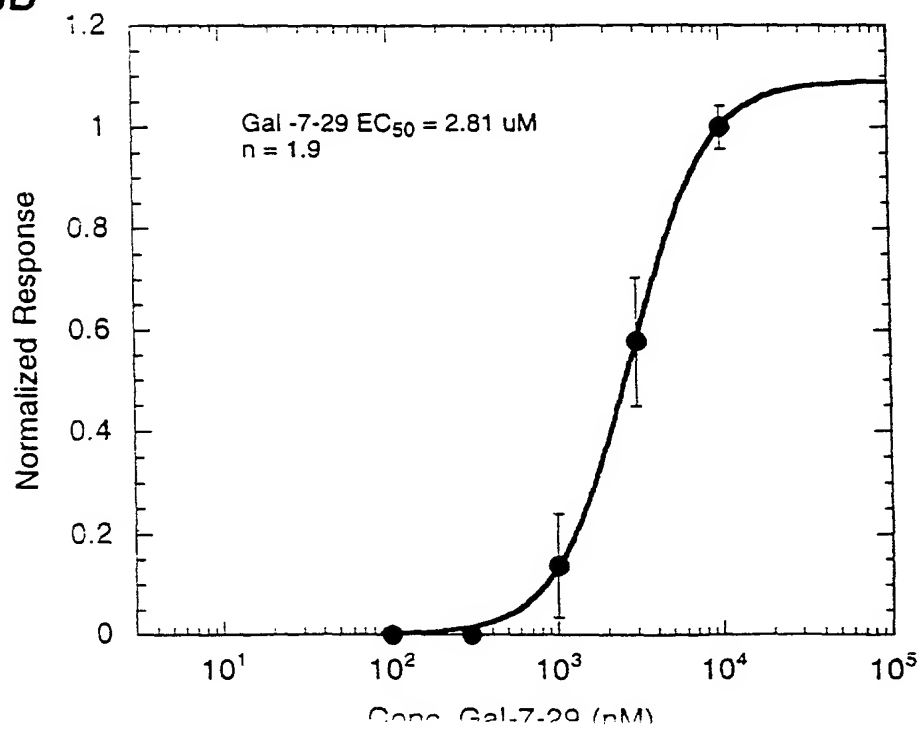


FIG. 8E

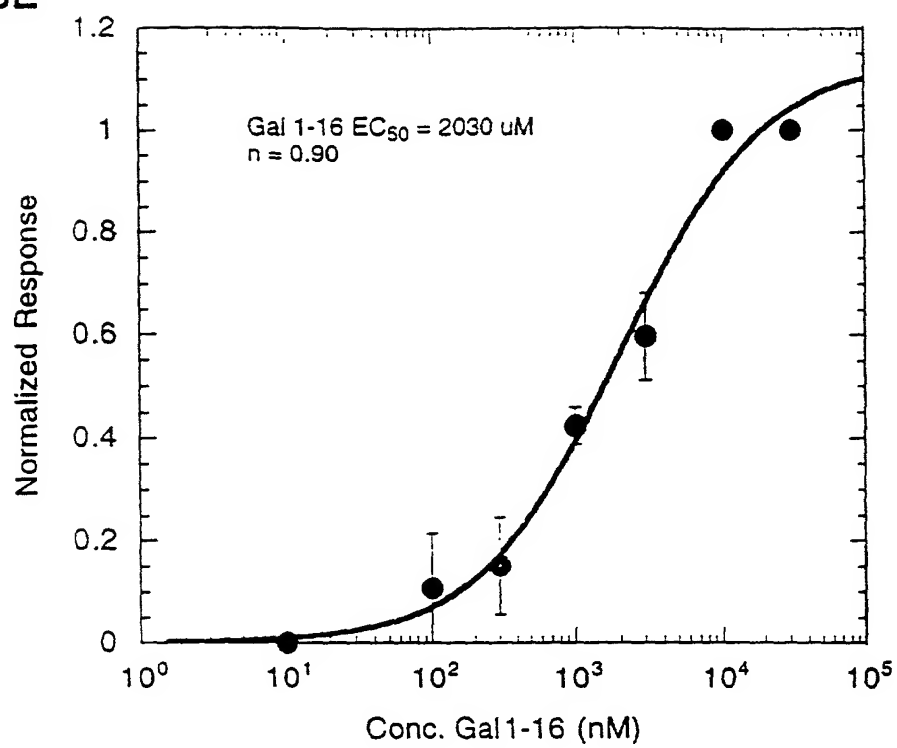


FIG. 8F

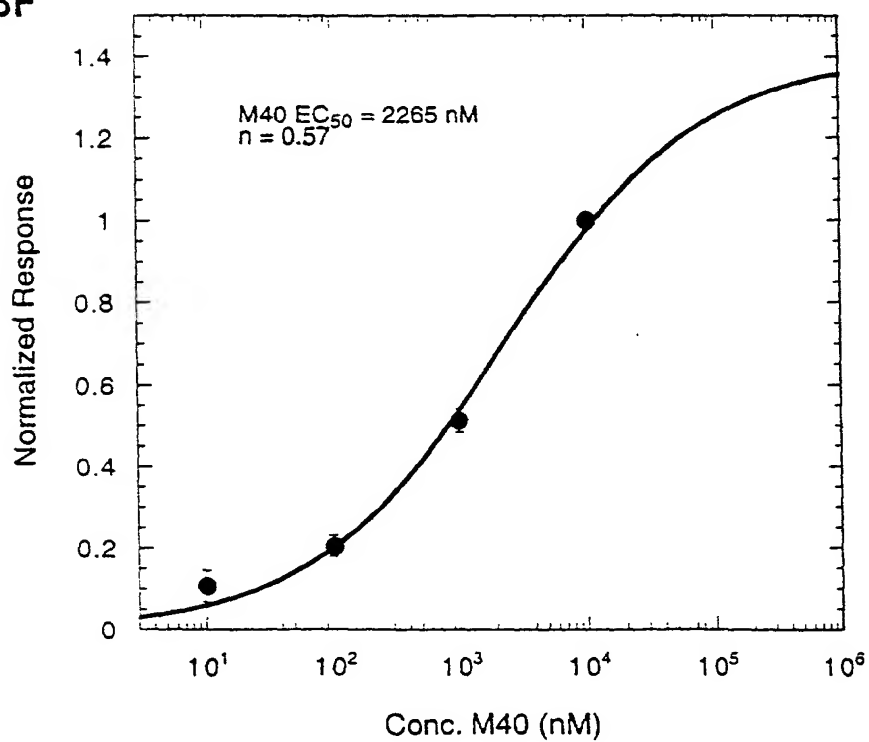


FIG. 9A

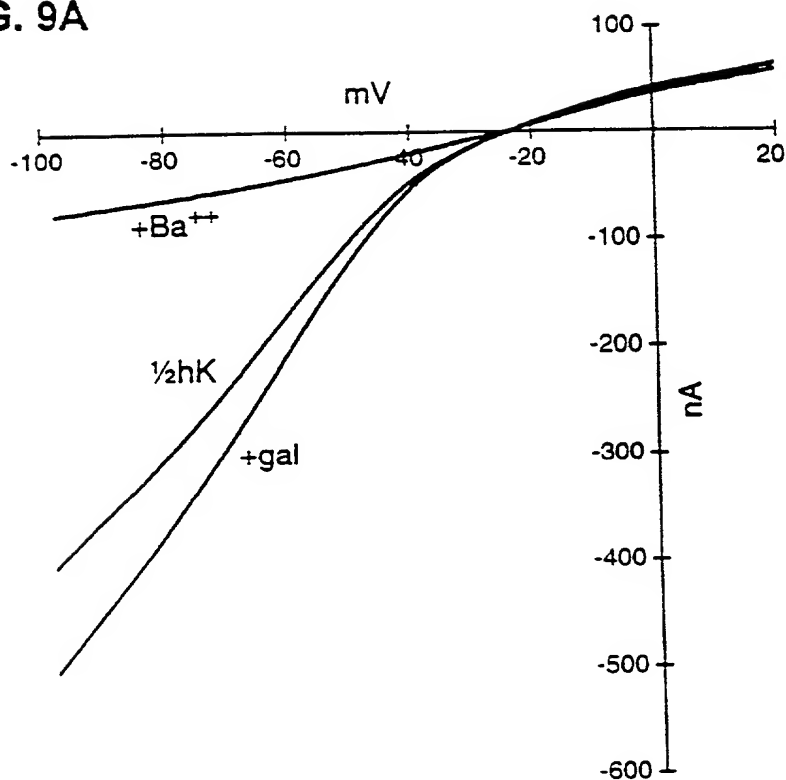


FIG. 9B

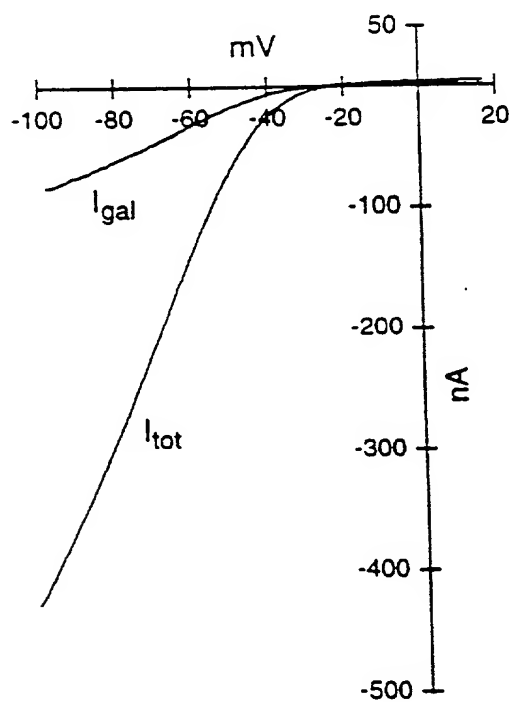


FIG. 10

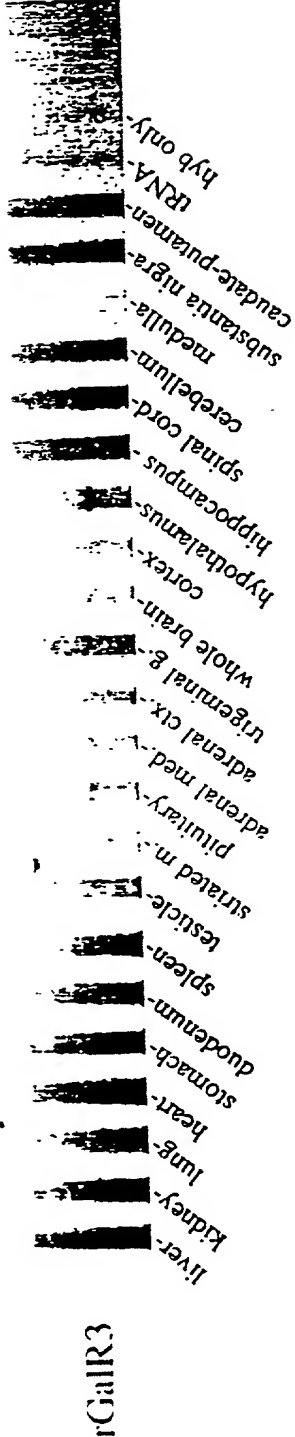


FIG. 11

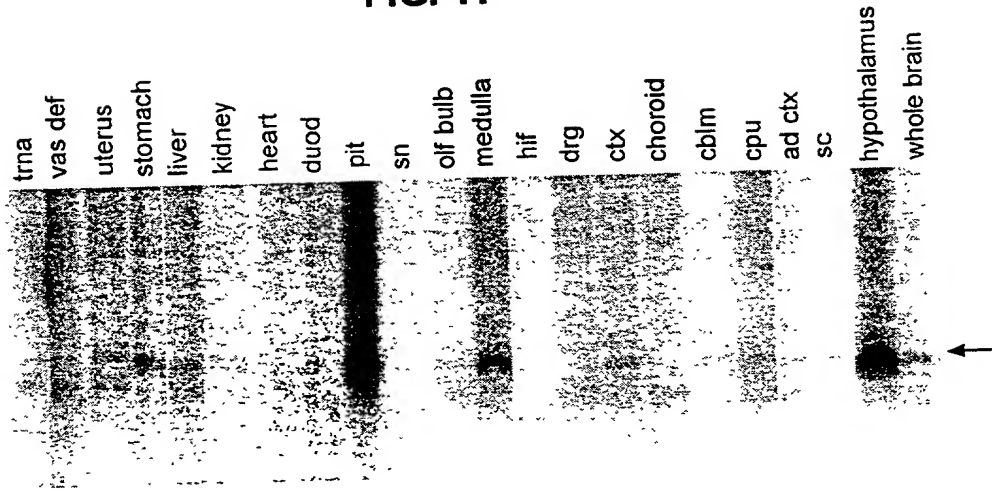


FIG. 12

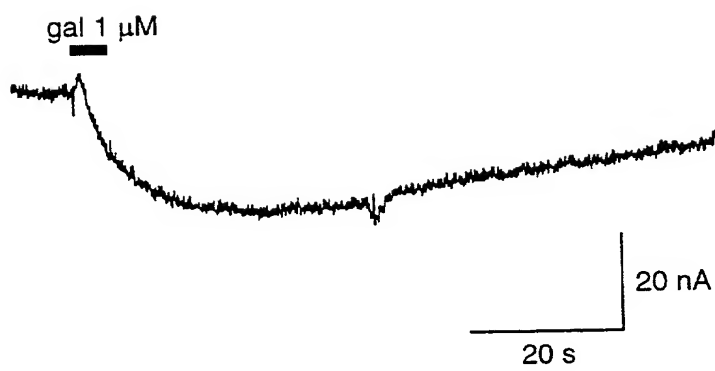


FIG. 13A

**hGALR3-LM #228
+/- Pertussis Toxin**

Guanine nucleotide effects

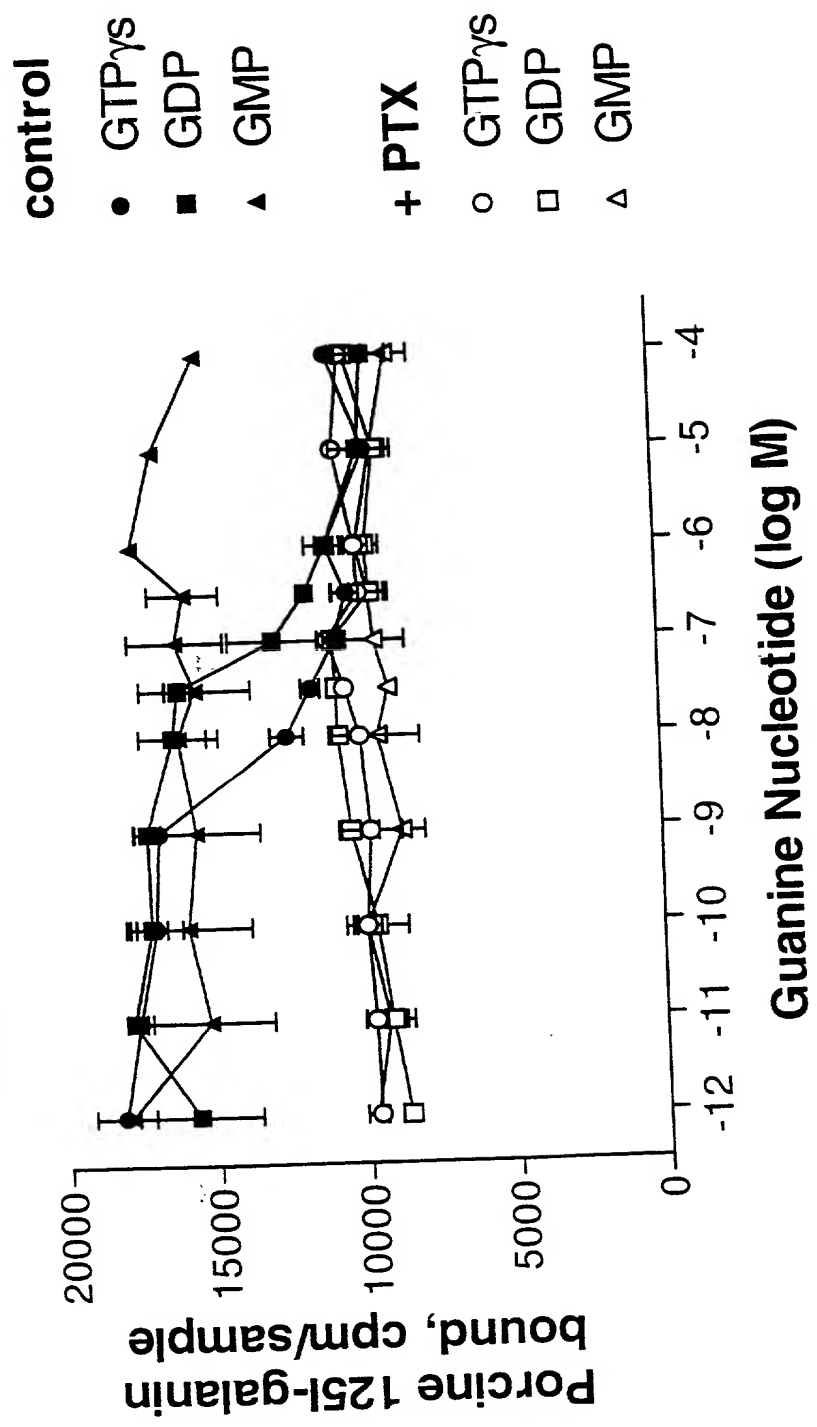


FIG. 13B
Nonspecific Binding
with 1 μ M p galanin

